

RAW SEQUENCE LISTING

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Application Serial Number: 09/485,650
Source: IFW/6
Date Processed by STIC: 8/22/05

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IFW16

RAW SEQUENCE LISTING

DATE: 08/22/2005

PATENT APPLICATION: US/09/485,650

TIME: 08:33:16

Input Set : A:\Cm1817.app

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3 <110> APPLICANT: Bettiol, Jean-Luc P.
 4 Thoen, Christiaan AJK
 6 <120> TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
 7 Soil Release Polymer
 9 <130> FILE REFERENCE: Mannanase and soil release polymer
 11 <140> CURRENT APPLICATION NUMBER: 09/485,650
 C--> 12 <141> CURRENT FILING DATE: 2000-04-05
 14 <150> PRIOR APPLICATION NUMBER: PCT/US98/12027
 15 <151> PRIOR FILING DATE: 1998-06-10
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1482
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus sp.
 26 <400> SEQUENCE: 1
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 28 ggaataatgg ggattacaac gtcccatca gcagcaagta caggctttta tgttgatggc 120
 29 aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
 30 gcttgggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240
 31 acgattcgta ttgttttatc agatggcggg caatgggaaa aagacgacat tgacaccatt 300
 32 cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat 360
 33 gccacgggtc gcgattcgcg cagtgtattt aatcgagccg ttgattattg gatagaaatg 420
 34 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480
 35 gggagttggg atggctcagc ttgggcccag ggctatatgt atgtcattcc gaagcttcgc 540
 36 gatgcccggc taacacacac cttaattggtt gatgcagcag gatgggggca atatccgcaa 600
 37 tctattcatg attacggaca agatgtgttt aatgcagatc cgtaaaaaaa tacgatgttc 660
 38 tccatccata tgtatgagta tgctgggtgg gatgctaaca ctgttagatc aaatattgat 720
 39 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780
 40 ggtgatgttg atgaagatac aatccttagt tattctgaag aaactggcac aggggtggctc 840
 41 gcttgggtctt ggaaaggcaa cagtaccgaa tgggactatt tagaccttc agaagactgg 900
 42 gctggtcaac atttaactga ttgggggaat agaattgtcc acggggccga tggcttacag 960
 43 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcacc tgaaccgcca 1020
 44 actgctacta ccttgatatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080
 45 accggtggcc cttgggtccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140
 46 gatgtaaatt taacctcaaa ttcttcacat gaactgtata gtgaacaaaag tcgtaatcta 1200
 47 cacggatact ctcagctcaa cgcaaccggt cgccatgcca attggggaaa tcccggtaat 1260
 48 ggcataaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcggtcct 1320
 49 tttaacacgta tcaatagctc caactcagga acaacgttat cttttgattt aaacaacatc 1380
 50 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt 1440
 51 ggtcaaaactg ctctatacgt tgataacggt actttaagat ag 1482
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 493

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56 <212> TYPE: PRT
57 <213> ORGANISM: Bacillus sp.
59 <400> SEQUENCE: 2
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63 Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala
64           20           25           30
66 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
67           35           40           45
69 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
70           50           55           60
72 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
73   65           70           75           80
75 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
76           85           90           95
78 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
79           100          105          110
81 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
82           115          120          125
84 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
85           130          135          140
87 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
88 145           150           155           160
90 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
91           165           170           175
93 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
94           180          185          190
96 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
97           195          200          205
99 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
100          210          215          220
102 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
103 225          230          235          240
105 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
106          245          250          255
108 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
109          260          265          270
111 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
112          275          280          285
114 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
115          290          295          300
117 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
118 305          310          315          320
120 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
121          325          330          335
123 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
124          340          345          350
126 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
127          355          360          365

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129 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
130      370                      375                      380
132 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
133 385                      390                      395                      400
135 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
136                      405                      410                      415
138 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
139                      420                      425                      430
141 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
142                      435                      440                      445
144 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His
145                      450                      455                      460
147 His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser
148 465                      470                      475                      480
150 Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg
151                      485                      490

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154 <210> SEQ ID NO: 3

155 <211> LENGTH: 1407

156 <212> TYPE: DNA

157 <213> ORGANISM: Bacillus sp.

159 <400> SEQUENCE: 3

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160 atgaaaaaaa agttatcaca gatttatcat ttaattatatt gcacacttat aataagtgtg 60
161 ggaataatgg ggattacaac gtcccatca gcagcaagta caggctttta tgttgatggc 120
162 aatacgttat atgacgcaaa tgggcagcca ttgtcatga gaggtattaa ccatggacat 180
163 gcttggtata aagacaccgc ttcaacagct attcctgccca ttgcagagca aggcgccaac 240
164 acgattcgta ttgttttatc agatggcggg caatgggaaa aagacgacat tgacaccatt 300
165 cgtgaagtca ttgagcttgc ggagcaaaat aaaatggtgg ctgtcgttga agttcatgat 360
166 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420
167 aaagatgcmc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480
168 gggagttggg atggctcagc ttgggcccag ggctatattg atgtcattcc gaagcttcgc 540
169 gatgccggct taacacacac cttaatggtt gatgcagcag gatgggggca atatccgcaa 600
170 tctattcatg attacggaca agatgtgttt aatgcagatc cgtaaaaaaa tacgatgttc 660
171 tccatccata tgtatgagta tgctggtggt gatgctaaca ctgttagatc aaatattgat 720
172 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780
173 ggtgatgttg atgaagatac aatccttagt tattctgaag aaactggcac aggggtggctc 840
174 gcttggtctt ggaaaggcaa cagtaccgaa tgggactatt tagacctttc agaagactgg 900
175 gctggtcaac atttaactga ttgggggaat agaattgtcc acggggccga tggcttacag 960
176 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcacc tgaaccgcca 1020
177 actgctacta cttgtgatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080
178 accggtggcc cttggtccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140
179 gatgtaaaatt taacctcaaa ttcttcacat gaactgtata gtgaacaaaag tcgtaatcta 1200
180 cacggatact ctcagctcaa cgcaaccgtt cgccatgccca attggggaaa tcccggtaat 1260
181 ggcatgaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcggctct 1320
182 ttacacgta tcaatagctc caactcagga acaacgttat cttttgattt aaacaacatc 1380
183 gaaaatatca tcatgttagg gaaatag 1407

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186 <210> SEQ ID NO: 4

187 <211> LENGTH: 468

188 <212> TYPE: PRT

189 <213> ORGANISM: Bacillus sp.

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191 <400> SEQUENCE: 4

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195 Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala
196           20           25           30
198 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
199           35           40           45
201 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
202           50           55           60
204 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
205   65           70           75           80
207 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
208           85           90           95
210 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
211           100          105          110
213 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
214           115          120          125
216 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
217           130          135          140
219 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
220  145          150          155          160
222 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
223           165          170          175
225 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
226           180          185          190
228 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
229           195          200          205
231 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
232           210          215          220
234 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
235  225          230          235          240
237 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
238           245          250          255
240 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
241           260          265          270
243 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
244           275          280          285
246 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
247           290          295          300
249 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
250  305          310          315          320
252 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
253           325          330          335
255 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
256           340          345          350
258 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
259           355          360          365
261 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
262           370          375          380

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264 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
265 385                      390                      395                      400
267 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
268                      405                      410                      415
270 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
271                      420                      425                      430
273 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
274                      435                      440                      445
276 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ile Ile
277 450                      455                      460
279 Met Leu Gly Lys
280 465
283 <210> SEQ ID NO: 5
284 <211> LENGTH: 1029
285 <212> TYPE: DNA
286 <213> ORGANISM: Bacillus sp.
288 <400> SEQUENCE: 5
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291 gaggttacag ccatgacaca ttttctatgg ctgaggctga tagaatccga agcgccaccg 180
292 ggcaatcgcc tgctatttat ggctgcgatt atgccagagg atggcttgaa acagcaaata 240
293 ttgaagattc aatagatgta agctgcaacg gcgatttaat gtcgtattgg aaaaatggcg 300
294 gaattccgca aatcagtttg caccctggcg accctgcttt tcagtcaggg cattttaaaa 360
295 caccgattac aaatgatcag tataaaaaaca tattagattc agcaacagcg gaagggaagc 420
296 ggctaaatgc catgctcagc aaaaattgctg acggacttca agagttggag aaccaaggtg 480
297 tgctgttct gttcaggccg ctgcatgaaa tgaacggcga atggttttgg tggggactca 540
298 catcatataa ccaaaaggat aatgaaagaa tctctctata taaacagctc tacaagaaaa 600
299 tctatcatta tatgaccgac acaagaggac ttgatcattt gatttgggtt tactctcccg 660
300 acgccaaccg agatttttaa actgattttt acccgggcgc gtcttacgtg gatattgtcg 720
301 gattagatgc gtattttcaa gatgcctact cgatcaatgg atacgatcag ctaacagcgc 780
302 ttaataaacc atttgctttt acagaaagtcg gcccgcaaac agcaaacggc agcttcgatt 840
303 acagcctgtt catcaatgca ataaaaaaca aatatcctaa aaccatttac tttctggcat 900
304 ggaatgatga atggagcgca gcagtaaaca aggggtgcttc agctttatat catgacagct 960
305 ggacactcaa caagggagaa atatggaatg gtgattcttt aacgccaatc gttgagtga 1020
306 tccgggatc 1029
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310 <211> LENGTH: 362
311 <212> TYPE: PRT
312 <213> ORGANISM: Bacillus sp.
314 <400> SEQUENCE: 6
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318 Ser Ala Val Leu Ala Lys Pro Ile Glu Ala His Thr Val Ser Pro Val
319 20 25 30
321 Asn Pro Asn Ala Gln Gln Thr Thr Lys Thr Val Met Asn Trp Leu Ala
322 35 40 45
324 His Leu Pro Asn Arg Thr Glu Asn Arg Val Leu Ser Gly Ala Phe Gly
325 50 55 60
327 Gly Tyr Ser His Asp Thr Phe Ser Met Ala Glu Ala Asp Arg Ile Arg

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